

EXHIBIT B

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	10	20	30	40	50	60
SEQID14	-----					
SEQID15	-----					
SEQID13	MAADGYLPDWLEDTLSEGIQWKLKPGPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD					
Prim.cons.	MAADGYLPDWLEDTLSEGIQWKLKPGPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD					
	70	80	90	100	110	120
SEQID14	-----					
SEQID15	-----					
SEQID13	KGSEPVNEADAAALEHDKAYDRQLDSCGNPYLKYNHADAEPQERLKEDTSFGGNLGRAVFQ					
Prim.cons.	KGSEPVNEADAAALEHDKAYDRQLDSCGNPYLKYNHADAEPQERLKEDTSFGGNLGRAVFQ					
	130	140	150	160	170	180
SEQID14	-----MAPGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
SEQID15	-----					
SEQID13	AKKRVLEPLGLVEEPVK2APGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
Prim.cons.	AKKRVLEPLGLVEEPVK2APGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD					
	190	200	210	220	230	240
SEQID14	SVPDPQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
SEQID15	-----MATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
SEQID13	SVPDPQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
Prim.cons.	SVPDPQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI					
	250	260	270	280	290	300
SEQID14	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
SEQID15	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
SEQID13	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
Prim.cons.	TTSTRTWALPTYNNHLYKQISSQSGASNDNHYPGYSTPWGYFDNRFHCHFSPRDWQRLI					
	310	320	330	340	350	360
SEQID14	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLSTVQVFTDSEYQLPYVLGSAHQG					
SEQID15	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLSTVQVFTDSEYQLPYVLGSAHQG					
SEQID13	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLSTVQVFTDSEYQLPYVLGSAHQG					
Prim.cons.	NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLSTVQVFTDSEYQLPYVLGSAHQG					
	370	380	390	400	410	420
SEQID14	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSOMLRGTGNNFTFSYTFEDVFP					
SEQID15	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSOMLRGTGNNFTFSYTFEDVFP					
SEQID13	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSOMLRGTGNNFTFSYTFEDVFP					
Prim.cons.	CLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPPSOMLRGTGNNFTFSYTFEDVFP					

	430	440	450	460	470	480
SEQID14	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
SEQID15	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
SEQID13	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
Prim.cons.	HSSYAH	SQSLDR	LMNPLID	QYLYLS	RNTNPS	GGTTTQ
	490	500	510	520	530	540
SEQID14	PCYRQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
SEQID15	PCYRQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
SEQID13	PCYRQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
Prim.cons.	PCYRQR	VSKTSAD	NNNSEY	SWTGAT	KYHLNG	RDSL
	550	560	570	580	590	600
SEQID14	IFGKQG	SEKTNV	DIEKVM	ITDEEE	IRTTNP	VATEQY
SEQID15	IFGKQG	SEKTNV	DIEKVM	ITDEEE	IRTTNP	VATEQY
SEQID13	IFGKQG	SEKTNV	DIEKVM	ITDEEE	IRTTNP	VATEQY
Prim.cons.	IFGKQG	SEKTNV	DIEKVM	ITDEEE	IRTTNP	VATEQY
	610	620	630	640	650	660
SEQID14	LPGMVW	QDRD	VYLQGP	IWAKI	PHTDGH	FHPSP
SEQID15	LPGMVW	QDRD	VYLQGP	IWAKI	PHTDGH	FHPSP
SEQID13	LPGMVW	QDRD	VYLQGP	IWAKI	PHTDGH	FHPSP
Prim.cons.	LPGMVW	QDRD	VYLQGP	IWAKI	PHTDGH	FHPSP
	670	680	690	700	710	720
SEQID14	FSAAKF	ASFITQ	YSTGQV	SVEIEW	ELQK	ENSKR
SEQID15	FSAAKF	ASFITQ	YSTGQV	SVEIEW	ELQK	ENSKR
SEQID13	FSAAKF	ASFITQ	YSTGQV	SVEIEW	ELQK	ENSKR
Prim.cons.	FSAAKF	ASFITQ	YSTGQV	SVEIEW	ELQK	ENSKR
	730					
SEQID14	SEPRPI	GTRYL	TRNL			
SEQID15	SEPRPI	GTRYL	TRNL			
SEQID13	SEPRPI	GTRYL	TRNL			
Prim.cons.	SEPRPI	GTRYL	TRNL			

Alignment data:

Alignment length: 735

Identity (*): 533 is 72.52 %

Strongly similar (:): 0 is 0.00 %

Weakly similar (.): 0 is 0.00 %

Different: 202 is 27.48 %

Sequence 0001: SEQID14 (598 residues). VP2

Sequence 0002: SEQID15 (533 residues). VP3

Sequence 0003: SEQID13 (735 residues). VP1

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